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Form 1449 (Modified)	Atty Docket No.	Application No.:
	MXGNP002X1/0159.210US	09/495,668
Information Disclosure Statement By Applicant	Applicant: Selifonov et al.	
	Filing Date	Group
(Use Several Sheets if Necessary)	February 1, 2000	1637

U.S. Patent Documents

Examiner Initial	No.	Patent No.	Date	Patentee	Class	Sub-class	Filing Date
	A1						
	A2						
	A3						
	A4						
	A5						
	A6						
	A7						
	A8						

Foreign Patent or Published Foreign Patent Application

Examiner Initial	No.	Document No.	Publication Date	Country or Patent Office	Class	Sub-class	Translation Yes	Translation No
	B1							
	B2							
	B3							
	B4							
	B5							

Other Documents

Examiner Initial	No.	Author, Title, Date, Place (e.g. Journal) of Publication
	C1	CS 262, Computational Genomics, Handout #1: Course Information, printed from: http://www.stanford.edu/class/cs, Spring 2003, 11 pages
	C2	Corpet et al., Browsing Protein Families Via the Rich Family Description Format," Bioinformatics, Vol. 15, No. 12, 1999, Pages 1020-1027
	C3	Mironov et al., "Computer Analysis of Transcription Regulatory Patterns in Completely Sequenced Bacterial Genomes," Nucleic Acids Research, Vol. 27, No. 14, 1999, Pages 2981-2989

Examiner	Date Considered 5-5-04

Examiner: Initial citation considered. Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.

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Other Documents

Examiner Initial	No.	Author, Title, Date, Place (e.g. Journal) of Publication
	C1	Aita et al., "Analysis of Local Fitness Landscape with a Model of the Rough Mt. Fuji-Type Landscape: Application to Prolyl Endopeptidase and Thermolysin," Biopolymers. Vol. 54, pp. 64-79, Accepted January 14, 2000
	C2	Hellberg et al., "The Prediction of Bradykinin Potentiating Potency of Pentapeptides. An Example of a Peptide Quantitative Structure-Activity Relationship," Acia Chemica Scandinaviea B 40, pp. 135-140, 1988
	C3	Bucht et al., "Optimising the Signal Peptide for Glycosyl Phosphatidylinositol Modification of Human Acetylcholinesterase Using Mutational Analysis and Peptide-Quantitative Structure-Activity Relationships," Biochimica et Biophysica Acta 1431, pp. 471-482, 1999
	C4	Sandberg et al., "Engineering Multiple Properties of a Protein by Combinatorial Mutagenesis," Proc. Natl. Acad. Sci. USA, Vol. 90, pp. 8367-8371, September 1993
	C5	Wrede et al., "Peptide Design Aided by Neural Networks: Biological Activity of Artificial Signal Peptidase I Cleavage Sites," Biochemistry, 37, pp. 3588-3593, 1998
	C6	Jill Damborsky, "Quantitative Structure-Function and Structure-Stability Relationships of Purposely Modified Proteins," Protein Engineering, Vol. 11, no. 1, pp. 21-30, 1998
	C7	Hellberg, et al., "Peptide Quantitative Structure–Activity Relationships, a Multivariate Approach," J. Med Chem, 30: pp 1126-1195, 1987
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	C9	Casari et al., "A Method to Predict Functional Residues in Proteins," Nat. Struct Biol., 2, pp. 171-178, 1995
	C10	Gogos et al., "Assignment of Enzyme Substrate Specificity by Principal Component Analysis of Aligned Protein Sequences: An Experiemental Test Using DNA Glycosylase Homologs," Proteins: Structure, Function, and Genetics, 40, pp. 98-105, 2000
	C11	Suzuki et al., "A Method for Detecting Positive Selection at Single Amino Acid Sites," Mol. Biol. Evol. 16 (10): pp. 1315-1328, 1999
	C12	Benner et al., "Amino Acid Substitution During Functionally Constrained Divergent Evolution of Protein Sequences," Protein Engineering, Vol. 7, No. 11, pp. 1323-1332, 1994

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	C13	Wu et al., "Discovering Empirically Conserved Amino Acid Substitution Groups in Databases of Protein Families," Proc. Int. Conf. Intell. Syst. Mol. Biol., 4, pp. 230-240, 1996
	C14	Adenot et al., "Peptides Quantitative Structure-Function Relationships: An Automated Mutation Strategy to Design Peptides and Pseudopeptides from Substitution Matrices," Journal of Molecular Graphics and Modelling, 17, pp. 292-309, 1999
	C15	Norinder et al., "A Quantitative Structure-Activity Relationship Study of Some Substance P-Related Peptides," J. Peptide Res., 49, pp. 155-162, 1997
	C16	Sandberg, "Deciphering Sequence Data a Multivariate Approach," Ph.D Thesis, Umea: Umea University, 78 pages, 1997
	C17	Eriksson et al., "Peptide QSAR on Substance P Analogues, Enkephalins and Bradykinins Containing L-and D-Amino Acids," Acta Chemica Scandinavica, 44, pp. 50-56, 1990
	C18	Ufkes eta l., "Further Studies on the Structure-Activity Relationships of Bradykinin-Potentiating Peptides," European Journal of Pharmacology, 79, pp. 155-158, 1982
	C19	Dobrynin et al., "Synthesis of Model Promoter for Gene Expression in Escherichia Coli," Symposium Series No. 7, pp. 365-376, 1980
	C20	Skinner et al., "Potential Use of Additivity of Mutational Effects in Simplifying Protein Engineering," Proc. Natl. Acad. Sci., Vol. 93, pp. 10753-10757, 1996
	C21	Aita et al., "Theory of Evolutionary Molecular Engineering Through Simultaneous Accumulation of Advantageous Mutations," J. Theor. Biol., 207, pp/ 543-556, 2000
	C22	Lathrop et al., "Global Optimum Protein Threading with Gapped Alignment and Empirical Pair Score Functions," J. Mol. Biol., 255, pp. 641-665, 1996
	C23	Hellberg et al., "A Multivariate Approach to QSAR," Ph.D. Thesis, Umea, Sweden: University of Umea: 1986
	C24	"Vector NTI Suite 7.0 User's Manual (portion) describing software believed to be available prior to February 1, 2000

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